

Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	1298	100.0	245	2	Q9KKE6	Q9KKE6	corynebacte
2	575	44.3	244	2	O69572	O69572	mycobacteri
3	566	43.6	247	2	O53516	O53516	mycobacteri
4	499	38.4	262	2	Q9S2M2	Q9S2M2	streptomyc
5	478	36.8	223	2	Q9L1B5	Q9L1B5	streptomyc
6	413	31.8	199	2	Q33970	Q33970	streptomyc
7	252.5	19.5	211	2	O67841	O67841	aquifex ae
8	246.5	19.0	247	2	Q9X219	Q9X219	thermotoga
9	226	17.4	823	2	O67119	O67119	aquifex ae
10	223	17.2	216	2	Q9PJT9	Q9PJT9	chlamydia m
11	217.5	16.8	264	2	Q9ZBS1	Q9ZBS1	streptomyc
12	215.5	16.6	195	2	Q9KCD7	Q9KCD7	bacillus ha
13	212.5	16.4	225	2	P74498	P74498	synecocyst
14	212.5	16.3	216	2	O84459	O84459	chlamydia t
15	202	15.6	212	10	Q9M0A2	Q9M0A2	arabidopsis
16	181	13.9	344	10	Q9LLF4	Q9LLF4	brassica na
17	173.5	13.4	259	2	O07807	O07807	mycobacteri
18	171.5	13.2	355	2	Q9WX09	Q9WX09	streptomyc
19	169.5	13.1	281	10	O9SD02	O9SD02	limnanthes

Qy 181 IDPLAFVKEHGLKPGCTYEAAARKLTDHVMFILADLTGQPYVDAYSKDVKNALEEGKGYPEG 240

Db 181 IDPLAFVKEHGLKPGTYEARKLTDHVMFLADLTGQPVYDAYSKDVKNALKEGKGYPEG 240
 QY 241 TAPSO 245
 Db 241 TAPSO 245

RESULT 2
 O69572 PRELIMINARY; PRT; 244 AA.
 AC O69572;
 DT 01-AUG-1998 (TRENBLrel. 07, Created)
 DT 01-AUG-1998 (TRENBLrel. 07, Last sequence update)
 DT 01-JUN-2000 (TRENBLrel. 14, Last annotation update)
 DE HYPOTHETICAL 26.8 KDA PROTEIN.
 GN MLCB268.24C.
 OS Mycobacterium leprae.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1769;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Brown D., Churcher C.M.;
 RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Parkhill J., Barrell B.G., Rajandream M.A.;
 RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93188700; PubMed=8446027;
 RA Eigmler K., Honore N., Woods S.A., Caudron B., Cole S.T.;
 RT *Use of an ordered cosmid library to deduce the genomic organization
 RT of Mycobacterium leprae.*;
 RL Mol. Microbiol. 7:197-206(1993).
 DR EMBL; AL022602; CAA18690.1; -;
 DR INTERPRO; IPR002123; -;
 DR PFAM; PF01553; Acyltransferase; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 244 AA; 26791 MW; 19F62F7BAC6BBB9 CRC64;

Query Match 44.3%; Score 575; DB 2; Length 244;
 Best Local Similarity 49.6%; Pred. No. 7.7e-44;
 Matches 111; Conservative 41; Mismatches 68; Indels 4; Gaps 2;

QY 5 WYRLKYLIGPFLRYNRPETEGKENIPAEAGAAIMASNHEAVMSDFYPLLCPLQLTTP 64
 Db 2 WYLFKYIFMGPALSVLGRPKVLEGVIPSSGPAILASNLAVADSFYPLVVRRIITEL 61
 QY 65 AKAEYFTSGIKGKQKWFSTSGVQVPLDRTADNADSLMTAKWLDKGLDGLFIYPEG 124
 Db 62 AKSEYFTGKLGWTSWYFRTAQVPIQDRTADTAELALNLAERLLGKGLIMTPEST 121
 QY 125 RSPDGRYKGTGMAYVAMETGTVIPVAMIGSRDANPTGSWFPKPAKVRKVGSPIDPL 184
 Db 122 RSPDGRYKGTGVARLTQTVIPVAMIGTVNPNPGRKMLRGRTVVRFGKPMD-- 179
 QY 185 APVKEHGLKPGTYEARKLTDHVMFLADLTGQPVYDAYSKDVKNALKEG 228
 Db 180 -FSRFEGL-AAGNRVIRVTDEVIVYELMELSGQYVDIYAASVK 221

RESULT 3
 O53516 PRELIMINARY; PRT; 247 AA.
 AC O53516;
 DT 01-JUN-1998 (TRENBLrel. 06, Created)
 DT 01-JUN-1998 (TRENBLrel. 06, Last sequence update)
 DT 01-JUN-2000 (TRENBLrel. 14, Last annotation update)
 DE HYPOTHETICAL 27.0 KDA PROTEIN.
 GN RV2182C OR MT0021.15C.
 OS Mycobacterium tuberculosis.

OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1773;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=H37RV;
 RX MEDLINE=98295987; PubMed=9634230;
 RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
 RA Gordon S.V., Eigmler K., Gas S., Barry C.E. III, Tekaiia F.,
 RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
 RA Davies K., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
 RA Hornsby T., Jagels K., Krohn A., McLean J., Moule S., Murphy L.,
 RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
 RA Rutter S., Seeger K., Skelton S., Squares S., Squires R., Sulston J.E.,
 RA Taylor K., Whitehead S., Barrell B.G.;
 RT *Deciphering the biology of Mycobacterium tuberculosis from the
 RT complete genome sequence.*;
 RL Nature 393:537-544(1998).
 DR EMBL; AL021957; CAA17486.1; -;
 DR TUBERCULIST; RV2182C; -;
 DR INTERPRO; IPR002123; -;
 DR PFAM; PF01553; Acyltransferase; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 247 AA; 26955 MW; FB1094228A340BDB CRC64;

Query Match 43.6%; Score 566; DB 2; Length 247;
 Best Local Similarity 47.8%; Pred. No. 5e-43;
 Matches 110; Conservative 43; Mismatches 73; Indels 4; Gaps 2;
 QY 5 WYRLKYLIGPFLRYNRPETEGKENIPAEAGAAIMASNHEAVMSDFYPLLCPLQLTTP 64
 Db 2 WYLFKYIFMGPFLTLGRPKVLEGVIPSSGPAILASNLAVADSFYPLVVRRIITEL 61
 QY 65 AKAEYFTSGIKGKQKWFSTSGVQVPLDRTADNADSLMTAKWLDKGLDGLFIYPEG 124
 Db 62 AKSEYFTGTGLKGNWIRWFYSVSGQVPIQDRTADTAELALNLAERLLGKGLIMTPEST 121
 QY 125 RSPDGRYKGTGMAYVAMETGTVIPVAMIGSRDANPTGSWFPKPAKVRKVGSPIDPL 184
 Db 122 RSPDGRYKGTGLARLALHTGVPIVAMIGTVNPNPGRKMLRGRTVVRFGKPMD-- 179
 QY 185 APVKEHGLKPGTYEARKLTDHVMFLADLTGQPVYDAYSKDVKNALKEG 234
 Db 180 -FSRFEGL-AGNHFTIRAVTDEVIVYELMELSGQYVDIYAASVKDGRNAG 227

RESULT 4
 O9S2M2 PRELIMINARY; PRT; 262 AA.
 AC O9S2M2;
 DT 01-MAY-2000 (TRENBLrel. 13, Created)
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TRENBLrel. 14, Last annotation update)
 DE HYPOTHETICAL 28.2 KDA PROTEIN.
 GN SC6E10.16C.
 OS Streptomyces coelicolor.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Streptomyces; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=1902;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2);
 RA Seeger K., Harris D.;
 RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2);
 RA James K.D., Parkhill J., Barrell B.G., Rajandream M.A.;
 RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2);